

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 09:30:59 ; Search time 4316 seconds  
(without alignments)  
12805.463 Million cell updates/sec

Title: US-09-494-297-1  
2274  
Perfect score: 1 atgaaaaacaagttcc.....ggataagaacaacgactag 2274  
Sequence:

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estlro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70.2	3.1	1101	29	CNS00396
2	69.4	3.1	1200	13	BX437758
3	66.8	2.9	1201	13	BX462660
4	65.2	2.9	960	13	BX346155

C	5	65.2	2.9	1201	9	AL536104	AL536104
C	6	64.2	2.8	687	12	BM169292	BM169292 EST571815
C	7	64.2	2.8	1056	13	BX415058	BX415058 BX415058
C	8	63.8	2.8	1169	13	BX448176	BX448176 BX448176
C	9	63.2	2.8	395	12	BM166601	BM166601 EST569124
C	10	63.2	2.8	964	13	BX341256	BX341256 BX341256
C	11	62.2	2.7	1201	13	BX439779	BX439779 BX439779
C	12	61.8	2.7	1098	13	BX377526	BX377526 BX377526
C	13	61.6	2.7	1044	13	BX415231	BX415231 BX415231
C	14	61.4	2.7	506	12	BM170012	BM170012 EST572535
C	15	61.4	2.7	770	12	BM169947	BM169947 EST572470
C	16	61.4	2.7	1101	29	CNS00EVL	AL069706 Drosophila
C	17	61	2.7	1201	29	CNS0167M	AL106396 Drosophila
C	18	60.8	2.7	1201	13	BX376097	BX376097 BX376097
C	19	60.6	2.7	998	13	BX436885	BX436885 BX436885
C	20	60.4	2.7	512	12	BM163047	BM163047 EST565570
C	21	60.4	2.7	999	13	BX380865	BX380865 BX380865
C	22	60.2	2.6	823	28	A2687380	A2687380 ENTL056TF
C	23	60.2	2.6	1092	29	CNS020K7	AL175696 Tetradon
C	24	60.2	2.6	1101	29	CNS01219	AL101595 Drosophila
C	25	60	2.6	994	13	BX414650	BX414650 BX414650
C	26	60	2.6	1101	29	CNS00EPO	AL069493 Drosophila
C	27	59.8	2.6	1008	13	BX398691	BX398691 BX398691
C	28	59.4	2.6	549	12	BM161900	BM161900 EST564423
C	29	59.4	2.6	747	12	BM169149	BM169149 EST571672
C	30	59.2	2.6	1032	29	CNS020IP	AL206746 Tetradon
C	31	58.6	2.6	762	12	BM166229	BM166229 EST568752
C	32	58.6	2.6	879	29	CNS01JRG	AL147405 Anopheles
C	33	58.6	2.6	1007	29	CNS06X9S	AL419462 T3 end of
C	34	58.6	2.6	1200	29	CNS016CO	AL106578 Drosophila
C	35	58.4	2.6	900	12	BM160720	BM160720 EST563243
C	36	58	2.6	632	9	AL514901	AL514901 AL514901
C	37	57.8	2.5	743	12	BJ446581	BJ446581 BJ446581
C	38	57.8	2.5	891	28	A2683582	A2683582 ENTK47TR
C	39	57.4	2.5	652	29	CNS03HOU	AL244551 Tetradon
C	40	57.4	2.5	1101	29	CNS0008B	AL063632 Drosophila
C	41	57.4	2.5	1201	9	AL514421	AL514421 AL514421
C	42	57.4	2.5	1201	9	AL536104	AL536104 AL536104
C	43	57.2	2.5	1124	13	BX436282	BX436282 BX436282
C	44	57.2	2.5	1200	13	BX415878	BX415878 BX415878
C	45	57.2	2.5	1201	13	BX446296	BX446296 BX446296

## ALIGNMENTS

RESULT 1  
CNS00396/c  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION  
AL063921  
AL063921.1 GI:4941778  
VERSION  
AL063921  
KEYWORDS  
SOURCE  
ORGANISM  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome project (BDGP).  
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mammosier in Pieter de Jong's laboratory in the Department of

## COMMENT

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
1. 1101  
Location/Qualifiers

/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR08K10"  
/clone\_1lb="RPCI-98"  
/note="end : TET3"  
BASE COUNT 201 a 64 c 131 g 202 t 503 others  
ORIGIN

Query Match 3.1%; Score 70.2; DB 29; Length 1101;  
Best Local Similarity 17.5%; Pred. No. 0.02;  
Matches 121; Conservative 286; Mismatches 283; Indels 1; Gaps 1;

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QY 107 TGATCTCGCTTGGTACTTCATGCTGCTGCTAAGACTGTTTGGTTTACTAGAAAT 166
D 1091 WDRTRKDDWMTKMTWMDKDRADDRWAGDADRWAMDDAGTWTATWMMWMTWMD 1032
QY 167 CCTGACGCGCAACGCAATTAATCCAGATTCAGATTCAGATTCAGATTCAGATTC 226
D 1031 TMDKMMWMTAAKTDTATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 972
QY 227 AATCTTATGTAAGAGGCGATCCATATATTAAGAGGTTAGAGTACACAGATTTAAGG 286
D 971 KDKKRDGDDGDKGKKAAKAKAKATWMDWMDKMDKMDKMDKMDKMDKMDKMDKMD 912
QY 287 TTAACTTAGAAGAGTAAAGTATCAAGTTATCTTATTAATTTAAGAAAGCATTC 346
D 911 DDDGKGADDDVGTGTDKDDKMDKMDKMDKMDKMDKMDKMDKMDKMDKMDKMD 852
QY 347 CTCTCGCATGATAGTAGTATTAAGAGTATTAAGAGTATTAAGAGTATTAAGAGT 406
D 851 DAADDDWMDRDMWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 792
QY 407 AATTTGAAGATTTAGCGATGCGCTTGAATTAAGAGGATGAGCTAATTCAGAGTTAC 466
D 791 AADRDAAATWTTTWTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 732
QY 467 GAGCTGTATGATTAATGAGATCCACAAATGCCATGATTAATGAGAGCTTGAAC 526
D 731 RTWKRKRKRDRDDADADDTARDDRRRGDDGAGKGTGKRKRKRDRDRATWDRDA 672
QY 527 CCTTGAATGCTATCAGATTAACAGAGGCGGATGATGATGATGATGATGATGATG 586
D 671 WMDAAWMTTDTDTDDWMDKRRRRKARRRRRT-TARAADWMTWMTWMTWMTWMT 613
QY 587 TTCTTAATCCAGATGAAGTTTAAAGAGTACAGAAAGTAACTGTTAGTACTCTC 646
D 612 DRMDRMDADWMTARADRDWMTARARARARARARARARARARARARARARAR 553
QY 647 AATTATCTTGATGCGTCAAGCTTTGAAGCACTGATGATCCGATTTGGCAACTAAA 706
D 552 AAAMWAMWMTATATWTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTT 493
QY 707 TGCCAAACAAAGTTCGCGATGATTTTTCAGCTAAGTATTTGAGTCCAGAGCAAG 766
D 492 AAAAAAAMWMTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTT 433
QY 767 ATAATATATAAGATACCAAAATCTTT 797
D 432 WMAATTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTT 402

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RESULT 2

BX437758  
LOCUS BX437758 1200 bp mRNA linear EST 15-MAY-2003  
DEFINITION BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YB01  
5-PRIME, mRNA sequence.  
ACCESSION BX437758  
VERSION BX437758.1 GI:30773605  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1200)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:  
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
Paradey Avenue Genoscope sequence ID: CS0CAP008CA01QPL.

FEATURES  
source  
1. 1200  
Location/Qualifiers

/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CS0CAP008YB01"  
/lssue\_type="THYMUS"  
/clone\_1lb="Homo sapiens THYMUS"  
/note="Vector: PCWVSPT6; 1st strand cDNA was primed  
with a NotI-oligo(dt) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the PCWVSPT 6 vector.  
Library was not normalized."  
BASE COUNT 515 a 30 c 71 g 310 t 274 others  
ORIGIN

Query Match 3.1%; Score 69.4; DB 13; Length 1200;  
Best Local Similarity 30.5%; Pred. No. 0.028;  
Matches 217; Conservative 148; Mismatches 339; Indels 7; Gaps 2;

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QY 1444 ATCAAAAAGTAATGGAAGGTTACAGGAGAAAAGACAGACATGATGATAGT 1503
D 357 ADATWATWMTTWTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 416
QY 1504 CTACAGTACAGACATTCGCTGGCGCTACGACGTTACATATATTTTACATGAT 1563
D 417 DTRAADWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 476
QY 1564 GCTGAATTTAGATAGATTAAGTAAAGACTATCATGTTTGGACATGAATGATG 1623
D 477 AARAAATWTTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 536
QY 1624 ACTTTAGACGTTGCTAAATCTGTAGATAGCTCAGATAGTAATCTCCACAGCTA 1683
D 537 TTWTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTTTWTGTT 596
QY 1684 ACTGACTTATTTCTTATTCGGAATACAAATATCAATCTCTATGGAACCTCAG 1743
D 597 TATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 654
QY 1744 TGCCAAACAAAGTTCGATGATTTTATGATTTGATGATGATGATGATGATGAT 1803
D 655 TMMWRDARRTATATATWTTTWTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 714
QY 1804 GTAACATATATTTAATGAGAAAACGCTAGCTGTTTACGCTGAGACAGATAA 1863
D 715 GAGAGAAATTTTTTATK-----AGARGATWTTTAMWMTTTRAGAGATTTT 769
QY 1864 GATTTCCATTTTGAATTTGAATTTAAATATTAACAGAAATGCTTCTCAACTGT 1923
D 1864 GATTTCCATTTTGAATTTGAATTTAAATATTAACAGAAATGCTTCTCAACTGT 1923

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Db 770 TAAATATTTTWWMAAGATDKAAAAAAMWTTWTAATAAAAAATTTWWAGARAATW 829  
 QY 1924 AAACAGATTAACCAACCTCGAATTTAAGATGTAAGACACATTAATTAACAT 1983  
 Db 830 TWAAMAAAAAAMAAAMAAATATATTTATATATATAKAAAAAATPAATTAARA 889  
 QY 1984 GCGAAGCTTACACTTCAAGGTTTACAGAGTTATCTTACCTGTCAAGAACCA 2043  
 Db 890 RRMGAAAAAATAAATAAATTTTATATAAAAAAATTTWAMWMAAARAAMAAAA 949  
 QY 2044 GATTCGAGGCTATAGGTTAAAGTTAATAGCAAGAGTAGCAAAATGCTACAGTTCA 2103  
 Db 950 GAARAGAAAMAAATTTTATATATATATAAAMWTTTWTWMAAAAAAMWDTT 1009  
 QY 2104 AAACAGATTAACAGATGATGACACTTGTCTTTGAAAAATTAAGAG 2154  
 Db 1010 TATWATWATWATAGAAATATARDATWRAATTAATWADAARAAAGAMATK 1060  
 RESULT 3  
 BX462660/c 1201 bp mRNA linear EST 22-MAY-2003  
 LOCUS BX462660 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA  
 DEFINITION clone CS0DH005YJ02 5-PRIME, mRNA sequence.  
 ACCESSION BX462660  
 VERSION BX462660.1 GI:31031442  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length CDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3370.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DH005DE01QPLcluster=3370.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL : Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DH005DE01QPL.  
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 /note="Vector: pCMVSPORT\_6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."  
 BASE COUNT 277 a 121 c 246 g 460 t 97 others  
 ORIGIN  
 Query Match 2.9%; Score 66.8; DB 13; Length 1201;  
 Best Local Similarity 38.1%; Pred. No. 0.08;  
 Matches 196; Conservative 51; Mismatches 268; Indels 0; Gaps 0;  
 QY 1753 GAAGTTAGTTGATATATTCGTATGAAGATAAAGAGTATACCTGTAACAT 1812  
 Db 1177 GGRDRKGGGGGAAAAAAMWTTTAAATTTTAAAAAATTTTAAAGAAARAAW 1118  
 QY 1813 AATTTACATTGAGAAAAACGGTGACTGTTAGCTGTGACAGAACTAAGATTCCAT 1872

Db 1117 WAAWAAAAAATAAAAAATGKATTTTTTTTATATATATATAAGAAWAGCGGGGAA 1058  
 QY 1873 TTTGAATTTGAATTAATAAATATATAGCAAGATTTCTTTCACAACTGTTAAACAGAT 1932  
 Db 1057 TWTATWATATATATAAAAAAATAAAAADTKTAAAAAGAGAGWTAAARAAATATTT 998  
 QY 1933 AAACAAACCTCGAATTTAAGATGTTAAGCAACCATTAATTTAAACATGGGAAGT 1992  
 Db 997 AAAATTAATAAAAAAATGKAAAAAATAAAAAAATAAAAAAATAAARAAATA 938  
 QY 1993 TTAACACTTCAAGTTTACCAAGAGTTATCTTCTTCTGCAAGAAACAGATTCTGAA 2052  
 Db 937 TTAAATTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 878  
 QY 2053 GCGTATAGGTTAAGTTAATATAGCAAGAGTAGCAAAATGCTACAGTTCAAAAAACGA 2112  
 Db 877 AAATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 818  
 QY 2113 ATACAGATGATGACACTTGTCTTTGAAAAATTAAGAGCCGTGTTCTACAGA 2172  
 Db 817 AAAAATTAATAAAAAATATATTTTAAATWTTAAATAAAAAAATAAAAAAATAAAAA 758  
 QY 2173 GTTCATCAAAAGATCAATGCTATCTAGCTTGTAGATGTTATCGCTGATCAGTTGGGG 2232  
 Db 757 TTTAAWATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 698  
 QY 2233 ATCTGGGAATTCACAGATTAAGATAAGAAACA 2267  
 Db 697 ATWTTTAAATTAATAAAAAATATAAAAAATAAAAAA 663  
 RESULT 4  
 BX346155/c 960 bp mRNA linear EST 05-MAY-2003  
 LOCUS BX346155 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
 DEFINITION Homo sapiens CDNA clone CS0DJ010YC14 5-PRIME, mRNA sequence.  
 ACCESSION BX346155  
 VERSION BX346155.1 GI:30373068  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 960)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length CDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0AJ010B807QPL.  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was  
 normalized."  
 BASE COUNT 284 a 100 c 80 g 366 t 130 others  
 ORIGIN



/mol\_type="mRNA"  
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 /dev\_stage="asexual blood stages"  
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 /clone\_1lb="PyBS"  
 /note="Vector: PAD-GAL4: At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with PY17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, unviral templates were treated with Pfu DNA polymerase and EcoRI adapters ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridZap arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybridZap vector and plasmid DNA

Query Match	2.8%	Score 64.2	DB 12	Length 687
Best Local Similarity	49.5%	Pred. No. 0.23		
Matches 165	Conservative	0	Mismatches 168	Indels 0
OY	1851 TGACAGACACTAAAGATTTCATTTTGAAGTTAAATAATAAGCAAGATTGCT	1910		
Db	109 TGTATGAAGTAAAAATGATGAGTAAAAAATGATGAGTAAAAAATGATGAGTAAAAA	168		
OY	1911 TTCTCAACACTTTAAACAGATTAACAACTCGAATTTAAGATGTAAGCAACCAT	1970		
Db	169 TGTATGAAGAAAAAAGCAAGAAAAAAGCAAGTAAAAAATGATGAGAAAAA	228		
OY	1971 TAAATTTAAACATGGGAAAGTTTAAACCTCAAGGTTTACCAGAGTTTATCTTACCT	2030		
Db	229 AGACGAGTAAAAAATGATGAGTAAAAAATGATGAGAAAAAAGCAAGTAAAAA	288		
OY	2031 TGTCAAGAAACAGATTCTGAAGCTTAAAGTTAAATTAATGACCAAGATGACAA	2090		
Db	289 TGACGAGTAAAAAATGATGAGTAAAAAATGATGAGTAAAAAAGCAAGTAAAAA	348		
OY	2091 TGTACACAGTTTCAAAAAACAGAAATTAACAGATGAGCACTTCTCTTTGAAAAATATA	2150		
Db	349 TGTATGAAGTAAAAATGATGAGTAAAAAATGACCAAGTAAAAAATGATGAGTAAAAA	408		
OY	2151 AGAGCTGTGTCTTCTACAGAGATTGATCAAAA	2183		
Db	409 TGACGAGTAAAAAATGATGAGTAAAAAAGGA	441		

  

RESULT 7	1056 bp	mRNA	linear	EST 15-MAY-2003
LOCUS	Bx415058			
DEFINITION	Bx415058 Homo sapiens THYMUS Homo sapiens cDNA CS0CAP004YG19			
ACCESSION	Bx415058			
VERSION	Bx415058.1	GI:30767520		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

Genoscope, Centre National de Séquençage  
BP 191 91006 Evry cedex - France  
Email: [segrete@genoscope.cns.fr](mailto:segrete@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact : Feng Liang Tech : [liangell@litech.com](mailto:liangell@litech.com) URL :  
<http://fulllength.invitrogen.com/> [invitrogen.com](http://invitrogen.com)  
Harvard Avenue Genoscope sequence ID : CS0CACP004AD10NPI.

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSOCCAP004YG19"
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/clone_id="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6, 1st strand cDNA was primed with a NotI-Oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

```

BASE COUNT	ORIGIN
454 a	53 c 56 g 318 t 175 others

Query Match	2.8%	Score 64.2	DB 13	length 1056
Best Local Similarity	33.9%	Pred. 0.23		
Matches	186	Conservative	91	Mismatches 263; Indels 9; Gaps 1;
QY	1694	ATTTCCTTATTCGCAATACACATTAATATATCATCTCTTATTTGGACACACATGCGATCCAG	1753	
Db	483	AAATTTTATATWAAATTTWAAAAAATAATTTWDKKKKWATATATAAAAAATAAAAAA	542	
QY	1754	AAGATTAAGTTGATATTTATTCGTATGGACAGATAAAAAAGATTAATCTGTAACATATA	1813	
Db	543	AAAATWATATATATATWTTATATKATATATAAAAAAATAATATATAAAAAATAAAATW	602	
QY	1814	ATTTAACATTTGAGAAAAACGCTGACCTGTTAGCTGGTGACAGAACTAAAGATTCCATT	1873	
Db	603	TTTWAAMAWGCTTTTTTTTCTTTTCTTTTWTWTAATATTTTWTATATATATATATATAT	662	
QY	1874	TTGAAATTTGCAATTAATAAATAATTAATAGCAGAAATGCTTTGCAAACTGTTAAACAGATA	1933	
Db	663	DATWAATATWTTWT RTGKAGWMAAAAAAKRTAKRTKRTAWMAAAAAAATAAAAAA	722	
QY	1934	AAACAAACCTTCGATTTTAAGATGTGTAAGCAACCACTTAATTTTAAACATGTGGAAAGTT	1993	
Db	723	AAAAAATAAAAAAATAATTTTTTTTTTAAAAAATAAATNNNNNNNTTAAAMWMMWTTT	782	
QY	1994	TAACACTTCAAGTTTACCGAAGATTAATCTTACTGTGCAAGAAACAGATTCGAG	2053	
Db	783	TTTTTTTTTMMWDDDDDDDTTTTTTTTTTTTTTTTTTTTTTMMWMMWMMWMMWMMW	842	
QY	2054	GCTATTAAGTTAAAGTTAATATAGCCACAGACAGAAATGCTACGCTTCCAAAAACAGAA	2113	
Db	843	WMMWMAWMAAAAAAATAATTTTWTAAATTTTATATAMWMAAAATGTTTRMAWMAAAAAA	902	
QY	2114	TAACAGTGTAGACACTGCTTT-----GAAATTAATVAAGACGCTGTGTC	2164	
Db	903	AAAAATTTAAAMAAAMWTTWMAAAWMMWTKNAAAAAATAAAAAAATAAAAAATTTTAT	962	
QY	2165	CTACAGAGTTGATCAACAAAGATCAATGCGATATCAGCTTTGATGCTATGCGTCGTCA	2224	
Db	963	TAGCAAGGTTTTTMAAAAAATAATGATMAATATATGKTTTWWAAADTTATATAATTA	1022	
QY	2225	GTTTGGGA 2233		
Db	1023	KTKKKKRA 1031		

[illegible]

Db	425	MAAAAAAAAAAGCGCCTTATWTCATATAAAMMTAAAMWACAAAAA	366
Oy	2095	ACAGTTTCAAAACAGCAATATACAGTGTATGACACTTGTCTTTGGAAATTAATTAAGAG	2155
Db	365	MAAAMAAWMAAAATATAMMAAAAAACACAGCTCCACAAAAAAMWACMAAAAAA	306
Oy	2155	CCCTTGTGCTCTACAGGAGTGTCATCAAAAGTCAATGCTTTCATAGCTTGT	2207
Db	305	MAAAMAAWMAAAATATAMMAAAATCTATRRAAACTGGGAATGTAATGTGCAT	253
RESULT 9			
LOCUS	BM166601	395 bp	mRNA linear EST 04-DEC-2001
DEFINITION	EST569124 PyBS Plasmodium yoelii yoelii cDNA clone pYCN037 5' end,		
ACCESSION	BM166601		
VERSION	BM166601.1		
KEYWORDS	EST.		
SOURCE	Plasmodium yoelii yoelii		
ORGANISM	Plasmodium yoelii yoelii		
REFERENCE	1 (bases 1 to 395)		
AUTHORS	Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdaya,A.B., Fraser,C.M. and Carucci,D.J.		
TITLE	Plasmodium yoelii EST project at TIGR		
JOURNAL	Unpublished		
COMMENT	Contact: Jane Carlton Parasite Genomics Group The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-530-9319 Fax: 301-838-0208 Email: carlton@tigr.org For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html Seq primer: ADF.		
FEATURES			
source	Location/Qualifiers		
	1..395		
	/organism="Plasmodium yoelii yoelii"		
	/mol_type="mRNA"		
	/strain="17XL"		
	/db_xref="taxon:73239"		
	/clone="pYCN037"		
	/dev_stage="Asexual blood stages"		
	/lab_host="E. coli XL-1 Blue"		
	/clone_lib="PyBS"		
	/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BAB/cby mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to Hybridzap arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pad-GAL4) was excised from the Hybridzap vector and plasmid DNA isolated."		
BASE COUNT	232 a	19 c	80 g 64 t
ORIGIN			
Query Match	2.8%	Score 63.2;	DB 12; Length 395;
Best Local Similarity	50.7%;	Pred. No. 0.34;	
Matches 152;	Conservative	0; Mismatches	148; Indels 0; Gaps 0;

OY		1850	GTGACAGACTGAAGATTCCATTTTGAAATTTGAATTAATAAATTAATAGCAGAATTGC	1909
Db		594	ATWMTAAATATTAATATTTTATTAATWTAAATTAATAATTAATAATAATTTTAAAAAAA	653
OY		1910	TTTCGCAACCGTTTAAACACATTAACAACCCTCGAATTTTAAAGATGGTAAACACCA	1969
Db		654	TAAATATTATTWTATTAATAAAAAAAAAAAAAAAAAAAWTAAWTAAATAAATAATATA	713
OY		1970	TTAATTTTAAACATGCGGAAGTTTAACTTCACAGGTTTCCGAAGGTTATCTTAGCC	2029
Db		714	TTATTAATTTTNNMAAATTAATATTTAAATAATTAAMATTAATAAAAAAAAAATTAAAAA	773
OY		2030	TTGTCAAAGAACAGATTCTGAGCGCTTAAGGTTTAAAGTTAATAGCCACAGACTAGCAA	2089
Db		774	AATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAANTWAATATATTATTAATAAATTAATAA	833
OY		2090	ATGCTACAGTTTCAAAAACGAGTAATACATGATGACACCTGCTTTGAAATATATA	2149
Db		834	AAATTAATTTTAAWWAAAAAAAAAATTAATAATTTTAAAAAATAAATAATTAWAAAAAA	893
OY		2150	AAGA 2153	
Db		894	TAAA 897	
RESULT 11				
BX439779		1201 bp	mRNA	linear EST 15-MAY-2003
DEFINITION	BX439779	Homo sapiens PLACENTA	Homo sapiens cDNA clone CSDBE014YF05	
LOCUS	BX439779	3-PRIME, mRNA sequence.		
ACCESSION	BX439779	GI:30771778		
VERSION	BX439779.1	EST.		
KEYWORDS	Homo sapiens (human)			
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 1201)			
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	unpublished			
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 3370.r For more information about this cluster, see <a href="http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSDBE014CC03NP1&amp;cluster=3370.r">http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSDBE014CC03NP1&amp;cluster=3370.r</a> . Contact : Feng liang Email : fliang@life tech.com URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Paraday Avenue genoscope sequence ID : CSDBE014CC03NP1. Location/Qualifiers 1..1201			
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source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSDBE014YF05" /tissue_type="PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."			
BASE COUNT	455 a 150 c 90 g 299 t	207 others		
ORIGIN				
Query Match	2.7%	Score 62.2	DB 13	Length 1201
Best Local Similarity	35.4%	Pred. No. 0.52		
Matches 194	Conservative 76	Misatches 276	Indels 2	Gaps 1



OY		1572	AGATPAGGATAAAGCTAAAGAAGCATCGTTTGCGACGACATGAATGATTACTTTCAGC	1631
Db		642	AATATATWTATTAATATWGTCTTGATATWTKTTTTAMATATATWTTTTTATATATTAAT	701
OY		1632	AGTTCCTAAATCCCTGGTAGAATACGCATAGTAATCCCTCACAGCTACTGACCCT	1691
Db		702	TWTWMAAAAAAATTTATTAATAATWTAATAAAAATTTWAHAATAAAAATWTAATTAAT	761
OY		1692	TGATTTCTCTTATCCGAAATCAATTAATCAATCTCTATTTGSACTCAGTGCATCC	1751
Db		762	ATPAATKTATWATTTWAAATTTATATTTTTPAATATATTTATWAAAAATTTATATMATW	821
OY		1752	AGAGATTACTTGATATATTTATTCGATGAGAGATPAAAAAGAGTTATACCTGTACTCA	1811
Db		822	TTTTTWTATWATATWTTWATTTTAAAAATWTAAMWMAAAAAAATTTTAAAAAWMT	881
OY		1812	TAAATTTAACATTGAGAAAAACGGGACTGGTTTGCTGCTGACAGAACTAAAGATTCCA	1871
Db		882	WWAATATWTTWATATWTTTAAWMAWMAATWTTTAA - WWAATMTAAATTWMAWMTTTPAA	939
OY		1872	TTTTGAAATTCATTTAAAAAATTAATTAACAGAAATGCTTCTCAAACTGTPTAAAAACA	1931
Db		940	AWTATATAAAAAATWATWATWATATATATAAAATTTAAAAATWMAATTTWMAAAAAAA	999
OY		1932	TAAAACAAACCTCGAATTTAAAGATGTGTAAGCAACCATTAATTTAAAAACATGGGAAAG	1991
Db		1000	AAWMAAAAAAATWATWTTAAAAATTTWMAAAATWATWMAAAWMAATTTTWTTTTAA	1059
OY		1992	TTTTAACCTTGACGGTTTACAGAGGTTATTCCTACCTGCCAAAGAAACAGANTTCGA	2051
Db		1060	TWMAATWTAAMAAAAATWTAAMAAAAAATAAAWMAATWMAAAATWMAAAATWMAAA	1119
OY		2052	AGGCTATTAAGGTTAAAGTTAATTAACCCAGAAAGTAGCAATCTCACGTTTCAAAAAACAG	2111
Db		1120	WAAWMNNTAAAAAAMARGAAMTTTAAAAAAMWTTAAAAAATTAATAAAWMAAAWMAAAW	1179
OY		2112	ATAAACA 2119	
Db		1180	WAAANMMA 1187	
RESULT 12				
BX377526/C				
LOCUS		BX377526	1098 bp	mRNA linear EST 08-MAY-2003
DEFINITION		BX377526 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION		BX377526		
VERSION		BX377526.1	GI:30460084	
KEYWORDS				
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE		1. (bases 1 to 1098)		
JOURNAL		Ll.W.B., Gruber,C.J., Jesse,J. and Polayes,D.		
COMMENT		Full-length cDNA libraries and normalization		
		Unpublished		
		Contact: Genoscope		
		Genoscope - Centre National de Sequencage		
		BP 191 91006 Evry cedex - France		
		Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
		Library was constructed by life technologies, a division of		
		Invitrogen. Contact : Feng Liang Email : fliang@life tech.com URL :		
		http://fulllength.invitrogen.com/Invitrogen Corporation 1600		
		Faraday Avenue genoscope sequence ID : CS0DI007DA04Op1.		
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Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8	DB 13	Length 1098		
Best Local Similarity	37.4%	Pred. No. 0.61				
Matches 168	Conservative	50	Mismatches 231	Indels 231	Gaps 0	
BASE COUNT	436 a	93 c	104 g	368 t	97 others	
ORIGIN						
Query Match	2.7%	Score 61.8				





REFERENCE 1 (bases 1 to 770)  
AUTHORS Carlton, V.M., Daly, T.M., Long, C.A., Bergman, L.W., Valdivia, A.B.,  
Fraser, C.M., and Carucci, D.J.  
TITLE Plasmodium yoelii EST project at TIGR  
JOURNAL Unpublished  
COMMENT Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlone@tigr.org

For clone info, please contact the Malaria Research and Reference  
Reagent Resource Center, ATCC  
<http://www.malaria.mr4.org/mr4pages/index.html>  
Seq primer: ADF.

FEATURES  
SOURCE Location/Qualifiers  
1..770

/organism="Plasmodium yoelii yoelii"  
/mol\_type="mRNA"  
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/clone="PYCP202"  
/dex\_stage="Asexual blood stages"  
/lab\_host="E. coli XL-1 Blue"  
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was  
collected from BALB/cBYJ mice infected with PY17XL  
parasites, and leukocytes removed by passage over  
microcrystalline cellulose columns. Total RNA was  
isolated using the guanidium isothiocyanate method, and  
mRNA isolated using oligo(dT)-cellulose chromatography.  
First strand cDNA synthesis was completed using a 50-base  
primer and reverse transcriptase in the presence of  
5-methyl dCTP. After second strand synthesis, uneven  
termini were treated with Pfu DNA polymerase and EcoRI  
adaptors ligated to the blunt ends. The sample was cleaved  
with XhoI and separated on a Sephacryl S-500 column.  
Size-fractionated cDNA was precipitated and ligated to  
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.  
After packaging, the phagemid vector (PAD-GAL4) was  
excised from the HybridZAP vector and plasmid DNA  
isolated."

BASE COUNT 379 a 64 c 131 g 196 t  
ORIGIN

Query Match 2.7%; Score 61.4; DB 12; Length 770;  
Best Local Similarity 49.8%; Pred. No. 0.72; Mismatches 156; Indels 0; Gaps 0;  
Matches 155; Conservative 0;

QY 1843 TTACCTGTGACAGACACTTAAGATTTCATTTCGAATTGAATTAATAAATAATATACCAA 1902  
DB 1 TTGAGAAAAAGCGAAGAAAAAGAGAGATTAATAAATGATGAAGAAAAAGACGAA 60  
QY 1903 GAATTCCTTCTCAACTGTTAAACAGATTAACCAACTCGAATTTAAAGATGTTAA 1962  
DB 61 GTAAAAAATGATGAATTAATAAATGATGAAGAAAAAGACGAGTAAATAAATGACGAA 120  
QY 1963 GCAACCATTAATTAATAACATGGGGAAGTTTACACTTCAGGTTTACCGAAGTTAT 2022  
DB 121 GTAAAAAATGATGAATTAATAAATGATGAAGTAAAGACGAGTAAATAAATGATGAA 180  
QY 2023 TCTTACCTGTCAAGAACAGATTCTGAAGCTATTAAGTTAAAGTTAATAGCCAGAA 2082  
DB 181 GTAAAAAATGATGAATTAATAAATGACGAGTAAATAAATGATGAAGTAAATAAATGACGAA 240  
QY 2083 GTACCAATGCTACAGTTTCAAAAAACGAAATTAACAAGTGAAGACACTTGCTTTGAA 2142  
DB 241 GTAAAAAATGATGAATTAATAAAGACGAGTAAATAAATGATGAAGTAAATAAATGATGAA 300  
QY 2143 AATTAATAAGA 2153  
DB 301 GTAAAAAATGATGA 311

Search completed: August 19, 2003, 13:15:48  
Job time : 4320 secs